



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/509,234

Source: 1655

Date Processed by STIC: 6-12-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED

JUL 09 2001

TECH CENTER 1600/2900

## Raw Sequence Listing Error Summary

**ERROR DETECTED****SUGGESTED CORRECTION**SERIAL NUMBER: 09/509, 234

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
    Wrapped Aminos   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☒ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino  
    Numbering       The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII       The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length   Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
    "bug"           A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
    (OLD RULES)   Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
    (NEW RULES)   Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9 ☐ Use of n's or Xaa's  
    (NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>  
    Response       Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☒ Use of <220>   Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
    "bug"           Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1655

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/509,234

DATE: 06/12/2001  
TIME: 15:26:01

Input Set : A:\es.txt  
Output Set : N:\CRF3\06122001\I509234.raw

Does Not Comply  
Corrected Diskette Needed  
See pp. 1-5

3 <110> APPLICANT: Vannuffel, Pascal  
4 Gala, Jean-Luc  
6 <120> TITLE OF INVENTION: GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS  
AND DEVICES  
7 FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS  
9 <130> FILE REFERENCE: VANM145.001APC  
W--> 10 <140> CURRENT APPLICATION NUMBER: 09/509,234  
C--> 11 <141> CURRENT FILING DATE: 2000-09-25  
13 <160> NUMBER OF SEQ ID NOS: 64  
14 <170> SOFTWARE: PatentIn version 3.0  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 1328  
19 <212> TYPE: DNA  
20 <213> ORGANISM: Staphylococcus femA Consensus Sequence  
22 <220> FEATURE:  
23 <221> NAME/KEY: misc\_feature  
24 <222> LOCATION: 1..1328  
25 <223> OTHER INFORMATION: n= any nucleotide  
27 <400> SEQUENCE: 1  
W--> 28 nnnnnnnnnn nnnanaatga antttacnaa tttnacngcn anagantttn gnnnntntac 60  
W--> 30 ngannnnnatg ncnanagnc atttnacnca nannnnngnn nantangann tnaannttgc 120  
W--> 32 nnannnnnnnn gannncann tagtnggnat naanaanaan nataangang tnattgcngc 180  
W--> 34 ntgnntntn acngcngtnc cngtnatgaa antnttnaan tanttttatt cnaannnggg 240  
W--> 36 nccngtnatn gattntnana annnaganct ngtncantnn ttctttaang anttnnnnaa 300  
W--> 38 ntatntnaaa nannannntn nnttatantn nnnntngan cctanntnn cntatcaata 360  
W--> 40 nnnnaatcat gangngann tnnngnnaa tgcnggnan gattggnnt tngatnannt 420  
W--> 42 nnnnnnnntn ggntntnanc annnnngntt nnnnannngn ttgancnnc tnnnncaa 480  
W--> 44 nngntnnncan tcngtntntan atttannnnn naaaannncn nanganntnn tnaannnnat 540  
W--> 46 ggatngnntn ngnaanngna anacnaaaaa agtnnanaan aatggngtna aagtnnnntt 600  
W--> 48 nntnnnnnaa gangannntc cnatnttng ntcattnatg gangatacnn cnganncnaa 660  
W--> 50 ngntntnnnn gatngngang annnttnta ntanaanngn tnnnnnnatt nnaaagannn 720  
W--> 52 ngtnntngtn ccnntngcnt atatnnantt tgatgantan ntnnnnnga tnnannnga 780  
W--> 54 nngnnannnn ntnantaaag annnaanaa agcnnntaan ganatngana aangncnga 840  
W--> 56 naanaaaaa gcnnnnaana annnnnnnaa nntnnaanan caantnnng cnaannanca 900  
W--> 58 aaantnnan gangnnannn nntnnaann nnancatggn aangaattac cnatntcngc 960  
W--> 60 ngntncttn ntatnaatc cntntgaagt ngtnntantan gcnggtgna cntcnaatnn 1020  
W--> 62 ntnnngncan ttngcnggna gntatgcnt ncaatggnn atgattaant atgcnttna 1080  
W--> 64 ncatnnnatn nanngntana attntatgg nnttagnggt nantttanng angangcnga 1140  
W--> 66 agatngnggn gtntnaant tnaaaaang ntannatgcn ganntntng antangttg 1200  
W--> 68 ngantntn aaacnnta anaancnt ntannnnnn tatannncan tnaaaaant 1260  
W--> 70 nnannnnann nnnntntann nannnnnnna nnnnnnatga aatttacaga 1320  
W--> 72 gttannn 1328  
75 <210> SEQ ID NO: 2  
76 <211> LENGTH: 35  
77 <212> TYPE: DNA  
78 <213> ORGANISM: artificial sequence  
80 <220> FEATURE:  
81 <223> OTHER INFORMATION: oligonucleotide

Line length error.  
Maximum of 72  
characters per line  
including spaces.

Too broad. What is the source  
of the genetic material in  
the artificial sequence? See  
#11 on the Error Summary 6/12/01  
Sheet.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/509,234

DATE: 06/12/2001  
TIME: 15:26:01

Input Set : A:\es.txt  
Output Set: N:\CRF3\06122001\I509234.raw

82 <221> NAME/KEY: misc\_feature  
83 <222> LOCATION: 1-35 ✓  
84 <223> OTHER INFORMATION: n= any nucleotide  
86 <400> SEQUENCE: 2  
W--> 87 anaatgaant ttacnaattt nacngcnana gantt 35  
90 <210> SEQ ID NO: 3  
91 <211> LENGTH: 20  
92 <212> TYPE: DNA  
93 <213> ORGANISM: artificial sequence  
W--> 94 <220> FEATURE: Missing mandatory <220> blank line feature. This feature must be present<sup>20</sup> whenever you have <221>, <222>, or <223> features. This error occurs throughout the sequence listing. Please review and correct.  
94 <223> OTHER INFORMATION: femS1 oligonucleotide OK  
96 <400> SEQUENCE: 3  
97 taatgaagtt tacaaaattt  
100 <210> SEQ ID NO: 4  
101 <211> LENGTH: 20  
102 <212> TYPE: DNA  
103 <213> ORGANISM: artificial sequence  
105 <220> FEATURE:  
106 <223> OTHER INFORMATION: femS2 oligonucleotide OK  
107 <221> NAME/KEY: misc\_feature  
108 <222> LOCATION: 14  
109 <223> OTHER INFORMATION: n= any nucleotide  
111 <400> SEQUENCE: 4  
W--> 112 taatgaagtt tacnaaaattt 20  
115 <210> SEQ ID NO: 5  
116 <211> LENGTH: 25  
117 <212> TYPE: DNA  
118 <213> ORGANISM: artificial sequence  
120 <220> FEATURE:  
121 <223> OTHER INFORMATION: oligonucleotide → see sequence #2.  
122 <221> NAME/KEY: misc\_feature  
123 <222> LOCATION: 1-25 ✓  
124 <223> OTHER INFORMATION: n= any nucleotide  
126 <400> SEQUENCE: 5  
W--> 127 atgncnnana gncatttnac ncana 25  
130 <210> SEQ ID NO: 6  
131 <211> LENGTH: 20  
132 <212> TYPE: DNA  
133 <213> ORGANISM: artificial sequence  
W--> 134 <220> FEATURE: Missing <220> feature  
134 <223> OTHER INFORMATION: femU1 oligonucleotide OK  
136 <400> SEQUENCE: 6  
137 tgccatatag tcatttacgc 20  
140 <210> SEQ ID NO: 7  
141 <211> LENGTH: 37  
142 <212> TYPE: DNA  
143 <213> ORGANISM: artificial sequence  
145 <220> FEATURE:  
146 <223> OTHER INFORMATION: oligonucleotide → see sequence #2

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/509,234

DATE: 06/12/2001  
TIME: 15:26:01

Input Set : A:\es.txt  
Output Set: N:\CRF3\06122001\I509234.raw

147 <221> NAME/KEY: misc\_feature  
148 <222> LOCATION: 1-37  
149 <223> OTHER INFORMATION: n= any nucleotide  
151 <400> SEQUENCE: 7  
W--> 152 tagtnggnat naanaanaa nataangang tnattgc 37  
155 <210> SEQ ID NO: 8  
156 <211> LENGTH: 35  
157 <212> TYPE: DNA  
158 <213> ORGANISM: artificial sequence  
160 <220> FEATURE:  
161 <223> OTHER INFORMATION: oligonucleotide → see sequence #2  
162 <221> NAME/KEY: misc\_feature  
163 <222> LOCATION: 1-35  
164 <223> OTHER INFORMATION: n= any nucleotide  
166 <400> SEQUENCE: 8  
W--> 167 gtncngttna tgaaantntt naantanttt tattc 35  
170 <210> SEQ ID NO: 9  
171 <211> LENGTH: 18  
172 <212> TYPE: DNA  
173 <213> ORGANISM: artificial sequence  
175 <220> FEATURE:  
176 <223> OTHER INFORMATION: oligonucleotide  
177 <221> NAME/KEY: misc\_feature  
178 <222> LOCATION: 1-18  
179 <223> OTHER INFORMATION: n= any nucleotide  
181 <400> SEQUENCE: 9  
W--> 182 aatgcngggn angattgg 18  
185 <210> SEQ ID NO: 10  
186 <211> LENGTH: 43  
187 <212> TYPE: DNA  
188 <213> ORGANISM: artificial sequence  
190 <220> FEATURE:  
191 <223> OTHER INFORMATION: oligonucleotide  
192 <221> NAME/KEY: misc\_feature  
193 <222> LOCATION: 1-43  
194 <223> OTHER INFORMATION: n= any nucleotide  
196 <400> SEQUENCE: 10  
W--> 197 gnaanngnaa nacnaaaaaa gttnanaana atggngtnaa agt 43  
200 <210> SEQ ID NO: 11  
201 <211> LENGTH: 18  
202 <212> TYPE: DNA  
203 <213> ORGANISM: artificial sequence  
W--> 204 <220> FEATURE: → missing <220> feature.  
204 <223> OTHER INFORMATION: fsq1S oligonucleotide  
206 <400> SEQUENCE: 11  
207 aaaaagttca aaaaatgg 18  
210 <210> SEQ ID NO: 12  
211 <211> LENGTH: 18  
212 <212> TYPE: DNA

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/509,234

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TIME: 15:26:01

Input Set : A:\es.txt  
Output Set: N:\CRF3\06122001\I509234.raw

213 <213> ORGANISM: artificial sequence → missing <220> feature

W--> 214 <220> FEATURE:

214 <223> OTHER INFORMATION: fsq2S oligonucleotide

216 <400> SEQUENCE: 12

217 aaaaagtaca aaaaatgg 18

220 <210> SEQ ID NO: 13

221 <211> LENGTH: 40

222 <212> TYPE: DNA

223 <213> ORGANISM: artificial sequence

225 <220> FEATURE:

226 <223> OTHER INFORMATION: oligonucleotide

227 <221> NAME/KEY: misc\_feature

228 <222> LOCATION: 1-40

229 <223> OTHER INFORMATION: n= any nucleotide

231 <400> SEQUENCE: 13

W--> 232 aagangannt nccnatnttn ngntcattna tggangatac 40

235 <210> SEQ ID NO: 14

236 <211> LENGTH: 20

237 <212> TYPE: DNA

238 <213> ORGANISM: artificial sequence

240 <220> FEATURE:

241 <223> OTHER INFORMATION: oligonucleotide

242 <221> NAME/KEY: misc\_feature

243 <222> LOCATION: 1-20

244 <223> OTHER INFORMATION: n= any nucleotide

246 <400> SEQUENCE: 14

W--> 247 tatatnnant ttgatganta 20

250 <210> SEQ ID NO: 15

251 <211> LENGTH: 32

252 <212> TYPE: DNA

253 <213> ORGANISM: artificial sequence

255 <220> FEATURE:

256 <223> OTHER INFORMATION: oligonucleotide

257 <221> NAME/KEY: misc\_feature

258 <222> LOCATION: 1-32

259 <223> OTHER INFORMATION: n= any nucleotide

261 <400> SEQUENCE: 15

W--> 262 aanganatng anaaangncc nganaaaaa aa 32

265 <210> SEQ ID NO: 16

266 <211> LENGTH: 18

267 <212> TYPE: DNA

268 <213> ORGANISM: artificial sequence

W--> 269 <220> FEATURE: → missing <220> feature

269 <223> OTHER INFORMATION: fsq3S oligonucleotide

271 <400> SEQUENCE: 16

272 aaagatatg aaaaacga 18

275 <210> SEQ ID NO: 17

276 <211> LENGTH: 20

277 <212> TYPE: DNA

See sequence #2

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/509,234

DATE: 06/12/2001  
TIME: 15:26:01

Input Set : A:\es.txt  
Output Set: N:\CRF3\06122001\I509234.raw

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278 <213> ORGANISM: artificial sequence
W--> 279 <220> FEATURE:
279 <223> OTHER INFORMATION: fsq4S oligonucleotide
281 <400> SEQUENCE: 17
282 aaagatattg aaaagagacc 20
285 <210> SEQ ID NO: 18
286 <211> LENGTH: 18
287 <212> TYPE: DNA
288 <213> ORGANISM: artificial sequence
W--> 289 <220> FEATURE:
289 <223> OTHER INFORMATION: fsq5S oligonucleotide
291 <400> SEQUENCE: 18
292 aaagatatcg agaaagac 18
295 <210> SEQ ID NO: 19
296 <211> LENGTH: 18
297 <212> TYPE: DNA
298 <213> ORGANISM: artificial sequence
W--> 299 <220> FEATURE:
299 <223> OTHER INFORMATION: fsq6S oligonucleotide
301 <400> SEQUENCE: 19
302 aaagacatcg acaagcgt 18
305 <210> SEQ ID NO: 20
306 <211> LENGTH: 22
307 <212> TYPE: DNA
308 <213> ORGANISM: artificial sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: oligonucleotide
312 <221> NAME/KEY: misc_feature
313 <222> LOCATION: 1-22
314 <223> OTHER INFORMATION: n= any nucleotide
316 <400> SEQUENCE: 20
W--> 317 ancatggnaa ngaattaccn at 22
320 <210> SEQ ID NO: 21
321 <211> LENGTH: 19
322 <212> TYPE: DNA
323 <213> ORGANISM: artificial sequence
W--> 324 <220> FEATURE:
324 <223> OTHER INFORMATION: fem1 oligonucleotide
326 <400> SEQUENCE: 21
327 gaacatggta atgaattac 19
330 <210> SEQ ID NO: 22
331 <211> LENGTH: 32
332 <212> TYPE: DNA
333 <213> ORGANISM: artificial sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: oligonucleotide
337 <221> NAME/KEY: misc_feature
338 <222> LOCATION: 1-32
339 <223> OTHER INFORMATION: n= any nucleotide

```

*Note* → The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

*Please Note:*  
*Note* → Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

file://C

6/12/01

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/509,234

DATE: 06/12/2001

TIME: 15:26:02

Input Set : A:\es.txt

Output Set: N:\CRF3\06122001\I509234.raw

L:10 M:283 W: Missing Blank Line separator, <140> field identifier  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:28 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:30 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:32 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:38 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:58 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:62 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:64 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:70 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:87 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:94 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:134 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:182 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:204 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:214 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:269 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:279 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:289 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:299 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:324 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/509,234

DATE: 06/12/2001

TIME: 15:26:02

Input Set : A:\es.txt

Output Set: N:\CRF3\06122001\I509234.raw

L:379 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:404 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:414 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:424 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:434 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:444 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:454 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:464 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:474 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:484 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:494 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:504 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:514 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:524 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:2384 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:2399 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:2409 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:2419 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:2429 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:2439 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:2449 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:2459 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:2469 M:258 W: Mandatory Feature missing, <220> FEATURE: